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(FILE 'HOME' ENTERED AT 15:13:01 ON 12 JAN 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN
2006

L1 24946 S STOP CODON OR STOP SIGNAL
L2 228 S L1 AND TRANSPOSON
L3 5 S L2 AND END SEQUENCE
L4 125 S (MODIFY OR CHANGE OR ALTER OR MUTATE OR TRUNCATE) AND END SEQ
L5 2 S L4 AND L1
L6 1 DUP REMOVE L5 (1 DUPLICATE REMOVED)
L7 9 S L4 AND TRANSPOSON
L8 3 DUP REMOVE L7 (6 DUPLICATES REMOVED)

=>

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NEWS 7 DEC 21 IPC search and display fields enhanced in CA/CAplus with the
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NEWS 8 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
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=> file medline caplus biosis scisearch
COST IN U.S. DOLLARS SINCE FILE TOTAL
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FILE 'SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN 2006

=> s stop codon or stop signal
L1 24946 STOP CODON OR STOP SIGNAL

=> s 11 and transposon
L2 228 L1 AND TRANSPOSON

=> s 12 and end sequence
2 FILES SEARCHED...
L3 5 L2 AND END SEQUENCE

=>

=> d ibib abs 1-5

L3 ANSWER 1 OF 5 MEDLINE on STN
ACCESSION NUMBER: 2003372847 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12907724
TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi.
AUTHOR: Lo Clive; Adachi Kiichi; Shuster Jeffrey R; Hamer John E; Hamer Lisbeth
CORPORATE SOURCE: Paradigm Genetics, Inc., 108 Alexander Drive, Research Triangle Park, NC 27709, USA.. clivel0@hkucc.hku.hk
SOURCE: Nucleic acids research, (2003 Aug 15) 31 (16) 4822-7.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200401
ENTRY DATE: Entered STN: 20030809
Last Updated on STN: 20040130
Entered Medline: 20040129

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular M. grisea CBS1 (encoding cystathionine beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

L3 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:837288 CAPLUS
DOCUMENT NUMBER: 139:333968
TITLE: Producing deletion derivatives of polypeptides using modified **transposon** with **stop codons** in all three reading frames
INVENTOR(S): Savilahti, Harri; Tieaho, Ville
PATENT ASSIGNEE(S): Finzymes Oy, Finland
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|------------|
| WO 2003087370 | A1 | 20031023 | WO 2003-FI285 | 20030414 |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |
| FI 2002000746 | A | 20031019 | FI 2002-746 | 20020418 |
| US 2005208616 | A1 | 20050922 | US 2005-511327 | 20050330 |
| PRIORITY APPLN. INFO.: | | | FI 2002-746 | A 20020418 |
| | | | WO 2003-FI285 | W 20030414 |

AB The present invention describes an *in vitro* transposition-based methodol. for generation of deletion derivs. of polypeptides. An artificial **transposon** containing at least partly within its **transposon** ends a modification with translation **stop codons** in three reading frames is provided. In the method, transposition complexes are assembled using the modified **transposon** and essentially random integrations into the target plasmid, containing a polypeptide coding nucleic acid of interest, are recovered as a plasmid pool. Subsequent manipulation steps including restriction enzyme digestions and ligation result in pools of mutant clones from which deletion derivs. of a polypeptide coding nucleic acid of interest and its resp. deletion polypeptides could be produced.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:616864 CAPLUS

DOCUMENT NUMBER: 139:318350

TITLE: The bacterial **transposon** Tn7 causes

premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi

Lo, Clive; Adachi, Kiichi; Shuster, Jeffrey R.; Hamer, John E.; Hamer, Lisbeth

CORPORATE SOURCE: Paradigm Genetics, Inc., Research Triangle Park, NC, 27709, USA

SOURCE: Nucleic Acids Research (2003), 31(16), 4822-4827

CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern anal. showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation.

Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi.

Similarly, a particular M.grisea CBS1 (encoding cystathionine β -synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for *in vivo* study of truncated gene products in filamentous fungi.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:563096 BIOSIS
DOCUMENT NUMBER: PREV200300564228
TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi.
AUTHOR(S): Lo, Clive [Reprint Author]; Adachi, Kiichi; Shuster, Jeffrey R.; Hamer, John E.; Hamer, Lisbeth
CORPORATE SOURCE: Department of Botany, The University of Hong Kong, Pokfulam Road, Hong Kong, China
clivel0@hkucc.hku.hk
SOURCE: Nucleic Acids Research, (August 15 2003) Vol. 31, No. 16, pp. 4822-4827. print.
ISSN: 0305-1048 (ISSN print).

DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Dec 2003
Last Updated on STN: 3 Dec 2003

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular M. grisea CBS1 (encoding cystathione beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

L3 ANSWER 5 OF 5 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:724714 SCISEARCH
THE GENUINE ARTICLE: 712DY
TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi
AUTHOR: Lo C (Reprint); Adachi K; Shuster J R; Hamer J E; Hamer L
CORPORATE SOURCE: Univ Hong Kong, Dept Bot, Pokfulam Rd, Hong Kong, Hong Kong, Peoples R China (Reprint); Univ Hong Kong, Dept Bot, Hong Kong, Hong Kong, Peoples R China; Paradigm Genet Inc, Res Triangle Pk, NC 27709 USA
COUNTRY OF AUTHOR: Peoples R China; USA
SOURCE: NUCLEIC ACIDS RESEARCH, (15 AUG 2003) Vol. 31, No. 16, pp. 4822-4827.
ISSN: 0305-1048.
PUBLISHER: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 33
ENTRY DATE: Entered STN: 5 Sep 2003
Last Updated on STN: 5 Sep 2003
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by

stop codons in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular *M.grisea* CBS1 (encoding cystathionine beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for *in vivo* study of truncated gene products in filamentous fungi.